

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/727,084A

DATE: 06/06/98
TIME: 13:51:14

INPUT SET: S26527.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING

ENTERED

- 1
- 2
- 3 (1) General Information:
- 4
- 5 (i) APPLICANT: Pulst, Stefan M
- 6
- 7 (ii) TITLE OF INVENTION: NUCLEIC ACID ENCODING SPINOCEREBELLAR
- 8 ATAXIA-2 AND PRODUCTS RELATED THERETO
- 9
- 10 (iii) NUMBER OF SEQUENCES: 18
- 11
- 12 (iv) CORRESPONDENCE ADDRESS:
- 13 (A) ADDRESSEE: Mueting, Raasch & Gebhardt, P.A.
- 14 (B) STREET: 119 North Fourth Street
- 15 (C) CITY: Minneapolis
- 16 (D) STATE: Minnesota
- 17 (E) COUNTRY: USA
- 18 (F) ZIP: 55401
- 19
- 20 (v) COMPUTER READABLE FORM:
- 21 (A) MEDIUM TYPE: Floppy disk
- 22 (B) COMPUTER: IBM PC compatible
- 23 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- 24 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- 25
- 26 (vi) CURRENT APPLICATION DATA:
- 27 (A) APPLICATION NUMBER: US 08/727,084
- 28 (B) FILING DATE: 08-OCT-1996
- 29 (C) CLASSIFICATION:
- 30
- 31 (viii) ATTORNEY/AGENT INFORMATION:
- 32 (A) NAME: McCormack, Myra H
- 33 (B) REGISTRATION NUMBER: 36,602
- 34 (C) REFERENCE/DOCKET NUMBER: 232.00010101
- 35
- 36 (ix) TELECOMMUNICATION INFORMATION:
- 37 (A) TELEPHONE: 612/305-1220
- 38 (B) TELEFAX: 612/305-1228
- 39
- 40
- 41
- 42 (2) INFORMATION FOR SEQ ID NO:1:
- 43
- 44 (i) SEQUENCE CHARACTERISTICS:
- 45 (A) LENGTH: 516 base pairs
- 46 (B) TYPE: nucleic acid

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47 (C) STRANDEDNESS: both
48 (D) TOPOLOGY: both
49
50 (ii) MOLECULE TYPE: DNA (genomic)
51
52
53
54 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
55
56 TTGGTAGCAA CGGAAACGGC GCGGCGCGT TTCGGCCCCG CTCCCGGCGG CTCCTTGATC 60
57
58 TCGGCGGGCC TCCCCGCCCC TCGTCGTCG TCCTTCTCCC CCTCGCCAGC CCGGGCGCCC 120
59
60 CTCCGGCCGC GCCAACCCGC GCCTCCCCGC TCGGCGCCCG TCGGTCCCCG CCGCGTTCCG 180
61
62 GCGTCTCCTT GCGCGGCCCC GCTCCCCGGT GTCCCCGCCC GCGGTGCGAG CCGGTGTATG 240
63
64 GGCCCTCAC CATGTCGCTG AAGCCCCAGC AGCAGCAGCA GCAGCAGCAG CAACAGCAGC 300
65
66 AGCAGCAACA GCAGCAGCAG CAGCAGCAGC AGCCGCCGCC CGCGGCTGCC AATGTCCGCA 360
67
68 AGCCCGGCGG CAGCGGCCTT CTAGCGTCGC CCGCGCCGC GCCTTCGCGG TCCTCGTCCT 420
69
70 CGGTCTCCTC GTCCTCGGCC ACGGCTCCCT CCTCGGTGGT CGCGGCGACC TCCGGCGGCG 480
71
72 GGAGGCCCCG CCTGGGCAGG TGGGTGTCGG CACCCC 516
73
74 (2) INFORMATION FOR SEQ ID NO:2:
75
76 (i) SEQUENCE CHARACTERISTICS:
77 (A) LENGTH: 4481 base pairs
78 (B) TYPE: nucleic acid
79 (C) STRANDEDNESS: both
80 (D) TOPOLOGY: both
81
82 (ii) MOLECULE TYPE: cDNA
83
84
85 (ix) FEATURE:
86 (A) NAME/KEY: CDS
87 (B) LOCATION: 163..4101
88
89
90 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
91
92 ACCCCCGAGA AAGCAACCCA GCGCGCCGCC CGCTCCTCAC GTGTCCCTCC CGGCCCCGGG 60
93
94 GCCACCTCAC GTTCTGCTTC CGTCTGACCC CTCCGACTTC CGGTAAAGAG TCCCTATCCG 120
95
96 CACCTCCGCT CCCACCCGGC GCCTCGGCGC GCCCGCCCTC CG ATG CGC TCA GCG 174
97 Met Arg Ser Ala
98 1
99

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100	GCC GCA GCT CCT CGG AGT CCC GCG GTG GCC ACC GAG TCT CGC CGC TTC	222
101	Ala Ala Ala Pro Arg Ser Pro Ala Val Ala Thr Glu Ser Arg Arg Phe	
102	5 10 15 20	
103		
104	GCC GCA GCC AGG TGG CCC GGG TGG CGC TCG CTC CAG CGG CCG GCG CGG	270
105	Ala Ala Ala Arg Trp Pro Gly Trp Arg Ser Leu Gln Arg Pro Ala Arg	
106	25 30 35	
107		
108	CGG AGC GGG CGG GGC GGC GGT GGC GCG GCC CCG GGA CCG TAT CCC TCC	318
109	Arg Ser Gly Arg Gly Gly Gly Gly Ala Ala Pro Gly Pro Tyr Pro Ser	
110	40 45 50	
111		
112	GCC GCC CCT CCC CCG CCC GGC CCC GGC CCC CCT CCC TCC CGG CAG AGC	366
113	Ala Ala Pro Pro Pro Pro Gly Pro Gly Pro Pro Pro Ser Arg Gln Ser	
114	55 60 65	
115		
116	TCG CCT CCC TCC GCC TCA GAC TGT TTT GGT AGC AAC GGC AAC GGC GGC	414
117	Ser Pro Pro Ser Ala Ser Asp Cys Phe Gly Ser Asn Gly Asn Gly Gly	
118	70 75 80	
119		
120	GGC GCG TTT CGG CCC GGC TCC CGG CGG CTC CTT GGT CTC GGC GGG CCT	462
121	Gly Ala Phe Arg Pro Gly Ser Arg Arg Leu Leu Gly Leu Gly Gly Pro	
122	85 90 95 100	
123		
124	CCC CGC CCC TTC GTC GTC GTC CTT CTC CCC CTC GCC AGC CCG GGC GCC	510
125	Pro Arg Pro Phe Val Val Val Leu Leu Pro Leu Ala Ser Pro Gly Ala	
126	105 110 115	
127		
128	CCT CCG GCC GCG CCA ACC CGC GCC TCC CCG CTC GGC GCC CGT GCG TCC	558
129	Pro Pro Ala Ala Pro Thr Arg Ala Ser Pro Leu Gly Ala Arg Ala Ser	
130	120 125 130	
131		
132	CCG CCG CGT TCC GGC GTC TCC TTG GCG CGC CCG GCT CCC GGC TGT CCC	606
133	Pro Pro Arg Ser Gly Val Ser Leu Ala Arg Pro Ala Pro Gly Cys Pro	
134	135 140 145	
135		
136	CGC CCG GCG TGC GAG CCG GTG TAT GGG CCC CTC ACC ATG TCG CTG AAG	654
137	Arg Pro Ala Cys Glu Pro Val Tyr Gly Pro Leu Thr Met Ser Leu Lys	
138	150 155 160	
139		
140	CCC CAG CAG CAG CAG CAG CAG CAG CAG CAA CAG CAG CAG CAG CAA CAG	702
141	Pro Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln	
142	165 170 175 180	
143		
144	CAG CAG CAG CAG CAG CAG CAG CCG CCG CCC GCG GCT GCC AAT GTC CGC	750
145	Gln Gln Gln Gln Gln Gln Gln Pro Pro Pro Ala Ala Ala Asn Val Arg	
146	185 190 195	
147		
148	AAG CCC GGC GGC AGC GGC CTT CTA GCG TCG CCC GCC GCC GCG CCT TCG	798
149	Lys Pro Gly Gly Ser Gly Leu Leu Ala Ser Pro Ala Ala Ala Pro Ser	
150	200 205 210	
151		
152	CCG TCC TCG TCC TCG GTC TCC TCG TCC TCG GCC ACG GCT CCC TCC TCG	846

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153	Pro Ser Ser Ser Ser Val Ser Ser Ser Ser Ala Thr Ala Pro Ser Ser	
154	215 220 225	
155		
156	GTG GTC GCG GCG ACC TCC GGC GGC GGG AGG CCC GGC CTG GGC AGA GGT	894
157	Val Val Ala Ala Thr Ser Gly Gly Gly Arg Pro Gly Leu Gly Arg Gly	
158	230 235 240	
159		
160	CGA AAC AGT AAC AAA GGA CTG CCT CAG TCT ACG ATT TCT TTT GAT GGA	942
161	Arg Asn Ser Asn Lys Gly Leu Pro Gln Ser Thr Ile Ser Phe Asp Gly	
162	245 250 255 260	
163		
164	ATC TAT GCA AAT ATG AGG ATG GTT CAT ATA CTT ACA TCA GTT GTT GGC	990
165	Ile Tyr Ala Asn Met Arg Met Val His Ile Leu Thr Ser Val Val Gly	
166	265 270 275	
167		
168	TCC AAA TGT GAA GTA CAA GTG AAA AAT GGA GGT ATA TAT GAA GGA GTT	1038
169	Ser Lys Cys Glu Val Gln Val Lys Asn Gly Gly Ile Tyr Glu Gly Val	
170	280 285 290	
171		
172	TTT AAA ACT TAC AGT CCG AAG TGT GAT TTG GTA CTT GAT GCC GCA CAT	1086
173	Phe Lys Thr Tyr Ser Pro Lys Cys Asp Leu Val Leu Asp Ala Ala His	
174	295 300 305	
175		
176	GAG AAA AGT ACA GAA TCC AGT TCG GGG CCG AAA CGT GAA GAA ATA ATG	1134
177	Glu Lys Ser Thr Glu Ser Ser Ser Gly Pro Lys Arg Glu Glu Ile Met	
178	310 315 320	
179		
180	GAG AGT ATT TTG TTC AAA TGT TCA GAC TTT GTT GTG GTA CAG TTT AAA	1182
181	Glu Ser Ile Leu Phe Lys Cys Ser Asp Phe Val Val Val Gln Phe Lys	
182	325 330 335 340	
183		
184	GAT ATG GAC TCC AGT TAT GCA AAA AGA GAT GCT TTT ACT GAC TCT GCT	1230
185	Asp Met Asp Ser Ser Tyr Ala Lys Arg Asp Ala Phe Thr Asp Ser Ala	
186	345 350 355	
187		
188	ATC AGT GCT AAA GTG AAT GGC GAA CAC AAA GAG AAG GAC CTG GAG CCC	1278
189	Ile Ser Ala Lys Val Asn Gly Glu His Lys Glu Lys Asp Leu Glu Pro	
190	360 365 370	
191		
192	TGG GAT GCA GGT GAA CTC ACA GCC AAT GAG GAA CTT GAG GCT TTG GAA	1326
193	Trp Asp Ala Gly Glu Leu Thr Ala Asn Glu Glu Leu Glu Ala Leu Glu	
194	375 380 385	
195		
196	AAT GAC GTA TCT AAT GGA TGG GAT CCC AAT GAT ATG TTT CGA TAT AAT	1374
197	Asn Asp Val Ser Asn Gly Trp Asp Pro Asn Asp Met Phe Arg Tyr Asn	
198	390 395 400	
199		
200	GAA GAA AAT TAT GGT GTA GTG TCT ACG TAT GAT AGC AGT TTA TCT TCG	1422
201	Glu Glu Asn Tyr Gly Val Val Ser Thr Tyr Asp Ser Ser Leu Ser Ser	
202	405 410 415 420	
203		
204	TAT ACA GTG CCC TTA GAA AGA GAT AAC TCA GAA GAA TTT TTA AAA CGG	1470
205	Tyr Thr Val Pro Leu Glu Arg Asp Asn Ser Glu Glu Phe Leu Lys Arg	

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	425	430	435	
206				
207				
208	GAA GCA AGG GCA AAC CAG TTA GCA GAA GAA ATT GAG TCA AGT GCC CAG			1518
209	Glu Ala Arg Ala Asn Gln Leu Ala Glu Glu Ile Glu Ser Ser Ala Gln			
210	440	445	450	
211				
212	TAC AAA GCT CGA GTG GCC CTG GAA AAT GAT GAT AGG AGT GAG GAA GAA			1566
213	Tyr Lys Ala Arg Val Ala Leu Glu Asn Asp Asp Arg Ser Glu Glu Glu			
214	455	460	465	
215				
216	AAA TAC ACA GCA GTT CAG AGA AAT TCC AGT GAA CGT GAG GGG CAC AGC			1614
217	Lys Tyr Thr Ala Val Gln Arg Asn Ser Ser Glu Arg Glu Gly His Ser			
218	470	475	480	
219				
220	ATA AAC ACT AGG GAA AAT AAA TAT ATT CCT CCT GGA CAA AGA AAT AGA			1662
221	Ile Asn Thr Arg Glu Asn Lys Tyr Ile Pro Pro Gly Gln Arg Asn Arg			
222	485	490	495	500
223				
224	GAA GTC ATA TCC TGG GGA AGT GGG AGA CAG AAT TCA CCG CGT ATG GGC			1710
225	Glu Val Ile Ser Trp Gly Ser Gly Arg Gln Asn Ser Pro Arg Met Gly			
226	505	510	515	
227				
228	CAG CCT GGA TCG GGC TCC ATG CCA TCA AGA TCC ACT TCT CAC ACT TCA			1758
229	Gln Pro Gly Ser Gly Ser Met Pro Ser Arg Ser Thr Ser His Thr Ser			
230	520	525	530	
231				
232	GAT TTC AAC CCG AAT TCT GGT TCA GAC CAA AGA GTA GTT AAT GGA GGT			1806
233	Asp Phe Asn Pro Asn Ser Gly Ser Asp Gln Arg Val Val Asn Gly Gly			
234	535	540	545	
235				
236	GTT CCC TGG CCA TCG CCT TGC CCA TCT CCT TCC TCT CGC CCA CCT TCT			1854
237	Val Pro Trp Pro Ser Pro Cys Pro Ser Pro Ser Ser Arg Pro Pro Ser			
238	550	555	560	
239				
240	CGC TAC CAG TCA GGT CCC AAC TCT CTT CCA CCT CGG GCA GCC ACC CCT			1902
241	Arg Tyr Gln Ser Gly Pro Asn Ser Leu Pro Pro Arg Ala Ala Thr Pro			
242	565	570	575	580
243				
244	ACA CGG CCG CCC TCC AGG CCC CCC TCG CGG CCA TCC AGA CCC CCG TCT			1950
245	Thr Arg Pro Pro Ser Arg Pro Pro Ser Arg Pro Ser Arg Pro Pro Ser			
246	585	590	595	
247				
248	CAC CCC TCT GCT CAT GGT TCT CCA GCT CCT GTC TCT ACT ATG CCT AAA			1998
249	His Pro Ser Ala His Gly Ser Pro Ala Pro Val Ser Thr Met Pro Lys			
250	600	605	610	
251				
252	CGC ATG TCT TCA GAA GGG CCT CCA AGG ATG TCC CCA AAG GCC CAG CGA			2046
253	Arg Met Ser Ser Glu Gly Pro Pro Arg Met Ser Pro Lys Ala Gln Arg			
254	615	620	625	
255				
256	CAT CCT CGA AAT CAC AGA GTT TCT GCT GGG AGG GGT TCC ATA TCC AGT			2094
257	His Pro Arg Asn His Arg Val Ser Ala Gly Arg Gly Ser Ile Ser Ser			
258	630	635	640	

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SEQUENCE VERIFICATION REPORT
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Original Text